

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggcccggc cgggccccca ttccggggccgg gcctcgctgc ggccggcgact 50

gagccaggct gggccgcgct cctgagtcct agagtcggcg cggcgccggca 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctcacaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtgcat gtgggtgcag 200

ccctgggagc actgtgtgttc tgccctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgggtggc actgggtggc accgatgcca ccctgtgctg 300

ctcctttctc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agataccaaa cagctgggtg acagctttgc tgagggccag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aacgcatccc tgaggctgca gcgcgtgcgt gtggcgagacg 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgacctgga 600

gccaacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg 750

cttgtttgat gtgcacagcg tcctgcgggt ggtgctgggt gcgaatggca 800

cctacagctg cctggtgcgc aaccccgctg tgcagcagga tgcgcacrgc 850

tctgtcacca tcacagggca gcctatgaca ttccccccag aggccctgtg 900
 ggtgaccgtg gggctgtctg tctgttcat tgcactgctg gtggccctgg 950
 ctttcgtgtg ctggagaaag atcaaacaga gctgtgagga ggagaatgca 1000
 ggagctgagg accaggatgg ggagggagaa ggctccaaga cagccctgca 1050
 gcctctgaaa cactctgaca gcaaagaaga tgatggacaa gaaatagcct 1100
 gaccatgagg accagggagc tgctaccctt ccctacagct cctaccctct 1150
 ggctgcaatg gggctgcact gtgagccctg cccccaacag atgcatcctg 1200
 ctctgacagg tgggctcctt ctccaaagga tgcgatacac agaccactgt 1250
 gcagccttat ttctccaatg gacatgattc ccaagtcacg ctgctgcctt 1300
 ttttcttata gacacaatga acagaccacc cacaacctta gttctctaag 1350
 tcactcctgcc tgctgcctta tttcacagta catacatttc ttagggacac 1400
 agtacctga ccacatcacc accctcttct tccagtgtg cgtggaccat 1450
 ctggctgcct tttttctcca aaagatgcaa tattcagact gactgacccc 1500
 ctgccttatt tcaccaaga cacgatgcat agtcaccccg gccttgtttc 1550
 tccaatggcc gtgatacact agtgatcatg ttcagccctg cttccacctg 1600
 catagaatct tttcttctca gacagggaca gtgcggcctc aacatctcct 1650
 ggagtctaga agctgtttcc tttccctcc ttcctccctg cccaagtga 1700
 agacagggca gggccaggaa tgctttgggg acaccgaggg gactgcccc 1750
 cccccacc atggtgctat tctggggctg gggcagtctt ttcctggctt 1800
 gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850
 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137

<211> 316

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> 233

<223> unknown amino acid

<400> 137

Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly

1	5	10	15
Ala Ala Leu Gly	Ala Leu Trp Phe Cys	Leu Thr Gly Ala Leu	Glu
20		25	30
Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
35		40	45
Ala Thr Leu Cys Cys	Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50		55	60
Ala Gln Leu Asn Leu	Ile Trp Gln Leu Thr	Asp Thr Lys Gln Leu	
65		70	75
Val His Ser Phe Ala	Glu Gly Gln Asp	Gln Gly Ser Ala Tyr Ala	
80		85	90
Asn Arg Thr Ala Leu	Phe Pro Asp Leu Leu	Ala Gln Gly Asn Ala	
95		100	105
Ser Leu Arg Leu Gln	Arg Val Arg Val Ala	Asp Glu Gly Ser Phe	
110		115	120
Thr Cys Phe Val Ser	Ile Arg Asp Phe Gly	Ser Ala Ala Val Ser	
125		130	135
Leu Gln Val Ala Ala	Pro Tyr Ser Lys Pro	Ser Met Thr Leu Glu	
140		145	150
Pro Asn Lys Asp Leu	Arg Pro Gly Asp Thr	Val Thr Ile Thr Cys	
155		160	165
Ser Ser Tyr Gln Gly	Tyr Pro Glu Ala Glu	Val Phe Trp Gln Asp	
170		175	180
Gly Gln Gly Val Pro	Leu Thr Gly Asn Val	Thr Thr Ser Gln Met	
185		190	195
Ala Asn Glu Gln Gly	Leu Phe Asp Val His	Ser Val Leu Arg Val	
200		205	210
Val Leu Gly Ala Asn	Gly Thr Tyr Ser Cys	Leu Val Arg Asn Pro	
215		220	225
Val Leu Gln Gln Asp	Ala His Xaa Ser Val	Thr Ile Thr Gly Gln	
230		235	240
Pro Met Thr Phe Pro	Pro Glu Ala Leu Trp	Val Thr Val Gly Leu	
245		250	255
Ser Val Cys Leu Ile	Ala Leu Leu Val Ala	Leu Ala Phe Val Cys	
260		265	270
Trp Arg Lys Ile Lys	Gln Ser Cys Glu Glu	Glu Asn Ala Gly Ala	
275		280	285
Glu Asp Gln Asp Gly	Glu Gly Glu Gly Ser	Lys Thr Ala Leu Gln	
290		295	300